



217770US0PCT.ST25
SEQUENCE LISTING

10 Rec'd PCT/JP

28 JUL 2004

<110> SHIBATA, TAKASHI
NOGUCHI, YUJI
YAMASHITA, MICHIO

<120> GENE ENCODING CYCLIC LIPOPEPTIDE ACYLASE AND EXPRESSION OF THE
SAME

<130> 217770US0PCT

<140> 10/019,282

<141> 2002-01-02

<150> PCT/JP00/04285

<151> 2000-06-28

<150> JP189644/1999

<151> 1999-07-02

<160> 76

<170> PatentIn version 3.2

<210> 1

<211> 5692

<212> DNA

<213> Streptomyces Sp.

<220>

<221> CDS

<222> (948)..(3362)

<400> 1
gaattccgga tggttggaga ggccgatcca gacggtgggc ggggcgaaga ggctgtcggc 60
caggcccgcgt tcgacgaggt cgaagatcga ggcggcggtcc ggaccgtcca ggatggtggt 120
ctccgcgccg accgccagat agggcagcag gaacacgtgc atctgggccg agtggttagag 180
cggcagggag tgcacggggc ggtcggtcgc ggcgaggccg agcgcggtga tcgcgctgac 240
gtactcgtgg accagggccc cgtgcgtcat catcgcgccc ttgggcaggg cgggtggtccc 300
ggaggtgtac agcagctgca ccaggtcgtc ggaggcgggc gggcgccgcg ggggtgaacgc 360
ccgttccgtc tccagggcgt cgagcagcga gccgggcgcg tcgcggagcg cgcgcaccgg 420
gagtcggcg gggagccgc cggcgaggtc cgggtcggtc aggacgagg aggagccgga 480
ctggtcgagg aggtaggcca ggtcgtcgc ggtgaggttc tggttgaccg gtacgtggac 540
gagaccggcc cgtgcgcagg cgaggaagcc gatcagatag gcgtcggagt tgtgcgcgta 600
ggcggccacc cggtcgccg gggcgagagc gtactcctcg gtgaggacgg cggcggccgt 660
ggagacggcg gcgtccagg agcggtaggt ccaggtccgg tcggcgtagc gcacggcggt 720
ccggtcgggg gtgcgccgg cgctgcgggt gaggacgccg tcgactgtgc tgctgcgtac 780
acctgtcatg gcgtgatcct gtgcgtccgg gccctcgggg gtcaagaggc tggataccga 840
ccagacgggt gacagcttcc cgggctccct ggctgagtga cgcttggccg tccgggcggt 900
ccggaccggc cgcgcccggt ccaccggtac cgctgggagg aaacacc ttg acg tta 956
Leu Thr Leu
1

217770US0PCT.ST25

cgc aac cgt ctg aga ctg ctc ggg gtc gcc ggt ctc gcc ctg ttc acc Arg Asn Arg Leu Arg Leu Leu Gly Val Ala Gly Leu Ala Leu Phe Thr 5 10 15	1004
gtg tcg gcg tcg ctg ccg cct gcc acc gcg tcc ggg acc cag gag acg Val Ser Ala Ser Leu Pro Pro Ala Thr Ala Ser Gly Thr Gln Glu Thr 20 25 30 35	1052
cgg cac ccg tcc ggg agc ggt ctt tcg gcc gtc atc cgg tac acg gag Arg His Pro Ser Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu 40 45 50	1100
tac ggc att ccg cac atc gtg gcg gag gac tac gcg cag ttg ggc ttc Tyr Gly Ile Pro His Ile Val Ala Glu Asp Tyr Ala Gln Leu Gly Phe 55 60 65	1148
ggc acc ggc tgg gcg cag gcc gcc gat cag gtg tgc acg ctg gcg gac Gly Thr Gly Trp Ala Gln Ala Ala Asp Gln Val Cys Thr Leu Ala Asp 70 75 80	1196
ggc ttc ctc acg gtg cgc ggg gag ccg tcg agg ttc ttc ggc ccg gac Gly Phe Leu Thr Val Arg Gly Glu Arg Ser Arg Phe Phe Gly Pro Asp 85 90 95	1244
gcc gcc acg gac tac tcc ctc tcc tcg gcg gcg acg aac ctc tcc agc Ala Ala Thr Asp Tyr Ser Leu Ser Ser Ala Ala Thr Asn Leu Ser Ser 100 105 110 115	1292
gac ctg tac ttc ccg ggc gtc cgc gac agc ggc acg gtg gag aag ctg Asp Leu Tyr Phe Arg Gly Val Arg Asp Ser Gly Thr Val Glu Lys Leu 120 125 130	1340
ctc aag gag ccc gcg ccc gcc ggt ccg agc agg gac gtc aag gag acg Leu Lys Glu Pro Ala Pro Ala Gly Pro Ser Arg Asp Val Lys Glu Thr 135 140 145	1388
atg cgc ggg ttc gcc gcc ggg tac aac gcg tgg atc gcg cag aac ccg Met Arg Gly Phe Ala Ala Gly Tyr Asn Ala Trp Ile Ala Gln Asn Arg 150 155 160	1436
atc acc gac ccc gcc tgc ccg ggc gcg tcc tgg gtg cgc ccg gtg acg Ile Thr Asp Pro Ala Cys Arg Gly Ala Ser Trp Val Arg Pro Val Thr 165 170 175	1484
gcg ctg gac gtg gcg gcg cgc ggc tac gcg ctg gcg gtg ctc ggc ggc Ala Leu Asp Val Ala Ala Arg Gly Tyr Ala Leu Ala Val Leu Gly Gly 180 185 190 195	1532
cag ggg ccg ggc atc gac ggc atc acc gcg gca cag ccg ccg acc gcc Gln Gly Arg Gly Ile Asp Gly Ile Thr Ala Ala Gln Pro Pro Thr Ala 200 205 210	1580
gct cct ccg gcg gcc ggg gtc acg ccc gag gag gcg gcg acg gcg gcg Ala Pro Pro Ala Ala Gly Val Thr Pro Glu Glu Ala Ala Thr Ala Ala 215 220 225	1628
gag ccg ctg ctg tcg acg cag aac gcg gac atg ggt tcc aac gcg gtg Glu Arg Leu Leu Ser Thr Gln Asn Ala Asp Met Gly Ser Asn Ala Val 230 235 240	1676
gcc ttc gac ggc tcc acg acg gtg aac ggg ccg ggg ctg ttg ctc ggc Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly Leu Leu Leu Gly 245 250 255	1724
aac ccg cac tac ccg tgg cag ggc gga cgc cgc ttc tgg cag gcg cag Asn Pro His Tyr Pro Trp Gln Gly Gly Arg Arg Phe Trp Gln Ala Gln 260 265 270 275	1772

217770US0PCT.ST25

cag acg atc ccc ggc gag ctg aac gtg tcg ggc gcg tcc ctg ctg ggc	1820
Gln Thr Ile Pro Gly Glu Leu Asn Val Ser Gly Ala Ser Leu Leu Gly	
280 285 290	
gcg acg acg atc tcg atc ggg cac aac gcc gat gtg gcg tgg agc cat	1868
Ala Thr Thr Ile Ser Ile Gly His Asn Ala Asp Val Ala Trp Ser His	
295 300 305	
acg gtc gcc acg ggc gtc acg ctg aat ctg cat cag ctc agc ctc gat	1916
Thr Val Ala Thr Gly Val Thr Leu Asn Leu His Gln Leu Ser Leu Asp	
310 315 320	
ccg gcc gac ccg acc gtc tat ctg gtg gac ggg aag gcg gag ccg atg	1964
Pro Ala Asp Pro Thr Val Tyr Leu Val Asp Gly Lys Arg Glu Arg Met	
325 330 335	
acg cag cgg acg gtg agc gtc ccg gtg aag ggc ggg gcc gac gtg acc	2012
Thr Gln Arg Thr Val Ser Val Pro Val Lys Gly Gly Ala Asp Val Thr	
340 345 350 355	
cgc acc cag tgg tgg acc cgc tac ggg ccg gtg gcc acc tcg atg ggc	2060
Arg Thr Gln Trp Trp Thr Arg Tyr Gly Pro Val Ala Thr Ser Met Gly	
360 365 370	
gcg ggg ctg ccg ttg ccg tgg acg gcg agc acg gcg tac gcg ctg aac	2108
Ala Gly Leu Pro Leu Pro Trp Thr Ala Ser Thr Ala Tyr Ala Leu Asn	
375 380 385	
gat ccg aac gcg acg aat ctg ccg atg gcg gac acc ggt ctg ggc ttc	2156
Asp Pro Asn Ala Thr Asn Leu Arg Met Ala Asp Thr Gly Leu Gly Phe	
390 395 400	
ggc aag gcc cgc tcc acg ggt gac gtc gag cgt gcg ctg cac ccg tcg	2204
Gly Lys Ala Arg Ser Thr Gly Asp Val Glu Arg Ala Leu His Arg Ser	
405 410 415	
cag ggc atg ccg tgg gtg aac acg atc gcg gcg gac ccg gcg ggt ccg	2252
Gln Gly Met Pro Trp Val Asn Thr Ile Ala Ala Asp Arg Ala Gly Arg	
420 425 430 435	
tcg ttc ttc gcg cag tcg cag gtg ctg ccg agg atc acc gac gcg ttg	2300
Ser Phe Phe Ala Gln Ser Gln Val Leu Pro Arg Ile Thr Asp Ala Leu	
440 445 450	
gcg gag cgc tgc tcg acc ccg ctg ggc ccg gcc acc tac ccc gct tcc	2348
Ala Glu Arg Cys Ser Thr Pro Leu Gly Arg Ala Thr Tyr Pro Ala Ser	
455 460 465	
ggc ctc gcg gtg ctg gac ggt tcg ccg acg gac tgc gcg ctg ggc agc	2396
Gly Leu Ala Val Leu Asp Gly Ser Arg Thr Asp Cys Ala Leu Gly Ser	
470 475 480	
gac ccg gac gcg gtg ccg ccg ggg atc ttc ggc ccg ggc ccg atg ccg	2444
Asp Pro Asp Ala Val Arg Pro Gly Ile Phe Gly Pro Gly Arg Met Pro	
485 490 495	
gtg ctg aag aac cag ccg tac gtg gag aac tcc aac gac agc gcg tgg	2492
Val Leu Lys Asn Gln Pro Tyr Val Glu Asn Ser Asn Asp Ser Ala Trp	
500 505 510 515	
ctg acc aat gcg gag ccg ccg ctg acc ggg tac gag ccg gtc ttc ggc	2540
Leu Thr Asn Ala Glu Arg Pro Leu Thr Gly Tyr Glu Arg Val Phe Gly	
520 525 530	
acg atc gcg acg ccc ccg tcg atg ccg acg cgc ggc gcg atc gag gac	2588
Thr Ile Ala Thr Pro Arg Ser Met Arg Thr Arg Gly Ala Ile Glu Asp	
535 540 545	

217770US0PCT.ST25

gtc Val	gcg Ala	tcg Ser 550	atg Met	gcg Ala	gac Asp	cgg Arg	ggc Gly 555	cgc Arg	ctc Leu	cgg Arg	gtc Val	ggg Gly 560	gac Asp	ctt Leu	cag Gln	2636
cgg Arg	cag Gln 565	cag Gln	ttc Phe	gcc Ala	aac Asn	cgt Arg 570	gcg Ala	ccg Pro	gcc Ala	ggg Gly	gat Asp 575	ctg Leu	gcc Ala	gcc Ala	tcc Ser	2684
gag Glu 580	gcc Ala	gcc Ala	aag Lys	tgg Trp	tgt Cys 585	gcg Ala	gcg Ala	ctg Leu	ccg Pro	ggc Gly 590	ggc Gly	acg Thr	gcc Ala	gtg Val	ggc Gly 595	2732
tcc Ser	gac Asp	gga Gly	acg Thr	ccg Pro 600	gtc Val	gac Asp	gtg Val	tgc Ser	gcg Ala 605	gcc Ala	tgc Cys	cgg Arg	gtg Val	ctg Leu 610	cgg Arg	2780
cgc Arg	tgg Trp	gac Asp	cgg Arg 615	acc Thr	gtg Val	gac Asp	agc Ser	gac Asp 620	agc Ser	cgg Arg	ggc Gly	gcg Ala	ctg Leu 625	ctc Leu	ttc Phe	2828
gac Asp	cgg Arg	ttc Phe 630	tgg Trp	cgg Arg	aag Lys	gcg Ala	tgc Ser 635	tgc Ser	gcg Ala	ccc Pro	gcc Ala	gcc Ala 640	gag Glu	ctg Leu	tgg Trp	2876
agg Arg	acg Thr 645	ccg Pro	ttc Phe	gat Asp	ccg Pro	gcc Ala 650	gac Asp	ccg Pro	gtg Val	cgc Arg	act Thr 655	ccg Pro	cgc Arg	ggc Gly	ctg Leu	2924
aac Asn 660	acg Thr	gcc Ala	gcg Ala	ccc Pro	gtc Val 665	ctg Leu	ggc Gly	agg Arg	gcc Ala	ctg Leu 670	gcg Ala	gac Asp	gcc Ala	gtg Val	gcg Ala 675	2972
gag Glu	ctg Leu	cgg Arg	gcg Ala 680	gcg Ala	ggc Gly	atc Ile	gcg Ala	ctg Leu	gac Asp 685	gcc Ala	ccg Pro	ctg Leu	ggc Gly	gag Glu 690	cac His	3020
cag Gln	ttc Phe	gtc Val 695	gtg Val	cgg Arg	aac Asn	ggc Gly	aag Lys	cgg Arg 700	ctc Leu	ccg Pro	atc Ile	ggc Gly 705	ggc Gly	ggg Gly	acg Thr	3068
gag Glu	tgc Ser	ctg Leu 710	ggc Gly	atc Ile	tgg Trp	aac Asn	aag Lys 715	acc Thr	gag Glu	ccg Pro	cag Gln	tgg Trp 720	aac Asn	gcg Ala	gcg Ala	3116
ggc Gly 725	ggc Gly	ggc Gly	tat Tyr	acg Thr	gag Glu	gtg Val 730	tgc Ser	tgc Ser	ggc Gly	tcc Ser	agc Ser 735	tac Tyr	atc Ile	cag Gln	gcg Ala	3164
gtc Val 740	ggc Gly	tgg Trp	gac Asp	gac Asp	agc Ser 745	cgc Arg	tgc Cys	ccg Pro	gtg Val	gcc Ala 750	cgg Arg	acg Thr	ctg Leu	ctg Leu	acg Thr 755	3212
tac Tyr	tcc Ser	cag Gln	tgc Ser	gag Glu 760	aac Asn	ccg Pro	aag Lys	tca Ser 765	ccg Pro	cac His	tac Tyr	agc Ser	gac Asp	cag Gln 770	acc Thr	3260
agg Arg	ctg Leu	tac Tyr	gcg Ala 775	ggt Gly	gag Glu	cgc Arg	tgg Trp	gtg Val 780	acg Thr	tcc Ser	cgg Arg	ttc Phe	tgc Cys 785	gag Glu	agg Arg	3308
gac Asp	atc Ile	gcg Ala 790	cgt Arg	tgc Ser	ccg Pro	gac Asp	ctg Leu 795	cgg Arg	gtg Val	gtg Val	cgg Arg	gtg Val	cac His	gag Glu	cgg Arg	3356
cgg Arg	tag	cgcggtgggc	ggacgggccc	gcccattccgc	ggcgagaagg	gcgtccgcct										3412

217770US0PCT.ST25

cggcgggagc cttctcacc gatgtgtcgt gaccgcgctc ccgggggagc cctcaccgag	3472
ccgccgaagg gcccggcggc cgaacccgtg accatgcgtg cgacgcatca cgctccgtcg	3532
gctccgccct ccgcccgcgc ccaggccagc tgcgcgtcgc tcagcggcgg gtcgaagcct	3592
tccgggaaca gcagcatccg cggctgcggc cacatgttct ccggtccgtg ttcctgacag	3652
tccagggcga ggagatgcgg cccgtccccg caggactcgt gccggtaggg gcggtcgtgc	3712
gcccggcaga aatagccgaa caccgcacag tggtcgtcgc cgcccggtcg gtggaagccg	3772
gggtcgtga cgatcacggt caccggctcc tgccggttga gccgagggat gggccgggga	3832
tcacgccaca acagtcgagg agggagcaca cgctcatctt ccccggggcc gagcccacgg	3892
gaagggggag cacggcgagg cgcctccgt cggcgtgatc gaccggggcc tcccgtcgc	3952
gggcggggcc tcccggacct gttgctctac agcgggcgt cgaagccctc ccagtacggt	4012
tcgcgcagcc gccgtttgta gagcttgccg ttggggtcgc ggggcatggc ggtgatgaag	4072
tcgaggctcc ggggtcgttt gtagccggcg agccgctcct cgagtgggc gaggatcgcg	4132
gcggcgagcg cgggtgacgg ctcgtggcca tcggccgggt cgacgacggc cttgacctcc	4192
tcgccgcggt cggcgtgggg gatgccgaag gcggcggcgt ccgcgacggc ggggtgggtg	4252
agcaggaccg actcgatctc ggcggggtag atgttgacct cgcccgcgat gatcatgtcg	4312
atcttgcggt cgcgaggaa gaggtagccg tcctcgtcca gcacgccgag gtcaccgacg	4372
gtgaagaagt cgccgatgcg gttcgtgcgg gtcttggtct cgtccttggt gtagctgaag	4432
ccgccggtgc tcatcttcat gtagacggtg cccagttcgc ctggcgggag gcggttgccg	4492
tcgtcgtcga agacggccag ttcgtgatc ggccaggcct tgccgacggt gccgggcttc	4552
ttcagccagt cctcggcggt ggcgaacgct ccccgccct cgctggccgc gtagtactcc	4612
tcgacgcagc tccccacca gtcgatcatg gcgcgtttga cgtggtcggg gcagggggct	4672
gccccgtgga tggcgtgccg catggaggag acgtcgtagc gggacctcac ctcgtcgggc	4732
agcgcgagca gccggtgaa ctgggtgggg accatgtggg tgtgggtgca gcggtgggcg	4792
tcgacgaggc gcagcatctc ctcgggcgac cagccgtcca tcaggaccag cgggtggccg	4852
atgtgcaggg cggcgccgc gaattggagt acggcggtgt ggtagagcgg cgagcagacc	4912
aggtggacgt tgtcgtcgaa cggccggatg ccgaagatgc cgaggaacct gccgaggtag	4972
gtctcctcgg ggcgtttgcc gggcaggggg cgccggatgc cgcgggggcg gccggtgggtg	5032
cccgaggtgt agttcatgac ccagccgagg gtgcggttct caggcggcgt ggcgggtgg	5092
ccttcgagga gttcgccca ggggcggcag ccggggaccg tgccgacgcc gtagcgggtg	5152
gtcgcgggca gttccgcctc gtcggcggcg gccgtcgcgg tggccgcgaa gcgttcgtgg	5212
gcgatcagga cgcgggcgcc ggagtcggcg acgatccagg cgatctcggg gccgacgagg	5272
tgggtggttg ccggcacgag gtagaagccg gcctgcgagg cggcgagggt ggcggtgagg	5332
agttcgacgc cgttgggcag gacgacggcg aacgcgtcgc cctcgcgcag tccggccgcg	5392
cgcaggccgt ggaccatgcg gttgacgtcg gcgtgcaggc ggcccgcgt ccactcctcg	5452

217770USOPCT.ST25

ccgtcggggg cgatcaggac ggtgcggtcg gggtcggctg cggcctgggc ccagaaaccg 5512
 ttgggcggct gggtcacgtg gcactccttc cggcgatgcg gttcatgcgg gtgacggccc 5572
 gttcgaagcc gcgggtcagg tcgtcgacga cggcccggac gctgcgttca ctggtcatcc 5632
 ggccgacgat ctgcccgcgc ggcgtgccga gcagctcgcc gacctcgta cttctggatcc 5692

<210> 2
 <211> 804
 <212> PRT
 <213> Streptomyces Sp.

<400> 2

Leu Thr Leu Arg Asn Arg Leu Arg Leu Leu Gly Val Ala Gly Leu Ala
 1 5 10 15

Leu Phe Thr Val Ser Ala Ser Leu Pro Pro Ala Thr Ala Ser Gly Thr
 20 25 30

Gln Glu Thr Arg His Pro Ser Gly Ser Gly Leu Ser Ala Val Ile Arg
 35 40 45

Tyr Thr Glu Tyr Gly Ile Pro His Ile Val Ala Glu Asp Tyr Ala Gln
 50 55 60

Leu Gly Phe Gly Thr Gly Trp Ala Gln Ala Ala Asp Gln Val Cys Thr
 65 70 75 80

Leu Ala Asp Gly Phe Leu Thr Val Arg Gly Glu Arg Ser Arg Phe Phe
 85 90 95

Gly Pro Asp Ala Ala Thr Asp Tyr Ser Leu Ser Ser Ala Ala Thr Asn
 100 105 110

Leu Ser Ser Asp Leu Tyr Phe Arg Gly Val Arg Asp Ser Gly Thr Val
 115 120 125

Glu Lys Leu Leu Lys Glu Pro Ala Pro Ala Gly Pro Ser Arg Asp Val
 130 135 140

Lys Glu Thr Met Arg Gly Phe Ala Ala Gly Tyr Asn Ala Trp Ile Ala
 145 150 155 160

Gln Asn Arg Ile Thr Asp Pro Ala Cys Arg Gly Ala Ser Trp Val Arg
 165 170 175

Pro Val Thr Ala Leu Asp Val Ala Ala Arg Gly Tyr Ala Leu Ala Val
 180 185 190

Leu Gly Gly Gln Gly Arg Gly Ile Asp Gly Ile Thr Ala Ala Gln Pro
 195 200 205

217770USOPCT.ST25

Pro Thr Ala Ala Pro Pro Ala Ala Gly Val Thr Pro Glu Glu Ala Ala
 210 215 220
 Thr Ala Ala Glu Arg Leu Leu Ser Thr Gln Asn Ala Asp Met Gly Ser
 225 230 235 240
 Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly Leu
 245 250 255
 Leu Leu Gly Asn Pro His Tyr Pro Trp Gln Gly Gly Arg Arg Phe Trp
 260 265 270
 Gln Ala Gln Gln Thr Ile Pro Gly Glu Leu Asn Val Ser Gly Ala Ser
 275 280 285
 Leu Leu Gly Ala Thr Thr Ile Ser Ile Gly His Asn Ala Asp Val Ala
 290 295 300
 Trp Ser His Thr Val Ala Thr Gly Val Thr Leu Asn Leu His Gln Leu
 305 310 315 320
 Ser Leu Asp Pro Ala Asp Pro Thr Val Tyr Leu Val Asp Gly Lys Arg
 325 330 335
 Glu Arg Met Thr Gln Arg Thr Val Ser Val Pro Val Lys Gly Gly Ala
 340 345 350
 Asp Val Thr Arg Thr Gln Trp Trp Thr Arg Tyr Gly Pro Val Ala Thr
 355 360 365
 Ser Met Gly Ala Gly Leu Pro Leu Pro Trp Thr Ala Ser Thr Ala Tyr
 370 375 380
 Ala Leu Asn Asp Pro Asn Ala Thr Asn Leu Arg Met Ala Asp Thr Gly
 385 390 395 400
 Leu Gly Phe Gly Lys Ala Arg Ser Thr Gly Asp Val Glu Arg Ala Leu
 405 410 415
 His Arg Ser Gln Gly Met Pro Trp Val Asn Thr Ile Ala Ala Asp Arg
 420 425 430
 Ala Gly Arg Ser Phe Phe Ala Gln Ser Gln Val Leu Pro Arg Ile Thr
 435 440 445
 Asp Ala Leu Ala Glu Arg Cys Ser Thr Pro Leu Gly Arg Ala Thr Tyr
 450 455 460
 Pro Ala Ser Gly Leu Ala Val Leu Asp Gly Ser Arg Thr Asp Cys Ala
 465 470 475 480

217770USOPCT.ST25

Leu Gly Ser Asp Pro Asp Ala Val Arg Pro Gly Ile Phe Gly Pro Gly
 485 490 495
 Arg Met Pro Val Leu Lys Asn Gln Pro Tyr Val Glu Asn Ser Asn Asp
 500 505 510
 Ser Ala Trp Leu Thr Asn Ala Glu Arg Pro Leu Thr Gly Tyr Glu Arg
 515 520 525
 Val Phe Gly Thr Ile Ala Thr Pro Arg Ser Met Arg Thr Arg Gly Ala
 530 535 540
 Ile Glu Asp Val Ala Ser Met Ala Asp Arg Gly Arg Leu Arg Val Gly
 545 550 555 560
 Asp Leu Gln Arg Gln Gln Phe Ala Asn Arg Ala Pro Ala Gly Asp Leu
 565 570 575
 Ala Ala Ser Glu Ala Ala Lys Trp Cys Ala Ala Leu Pro Gly Gly Thr
 580 585 590
 Ala Val Gly Ser Asp Gly Thr Pro Val Asp Val Ser Ala Ala Cys Arg
 595 600 605
 Val Leu Arg Arg Trp Asp Arg Thr Val Asp Ser Asp Ser Arg Gly Ala
 610 615 620
 Leu Leu Phe Asp Arg Phe Trp Arg Lys Ala Ser Ser Ala Pro Ala Ala
 625 630 635 640
 Glu Leu Trp Arg Thr Pro Phe Asp Pro Ala Asp Pro Val Arg Thr Pro
 645 650 655
 Arg Gly Leu Asn Thr Ala Ala Pro Val Leu Gly Arg Ala Leu Ala Asp
 660 665 670
 Ala Val Ala Glu Leu Arg Ala Ala Gly Ile Ala Leu Asp Ala Pro Leu
 675 680 685
 Gly Glu His Gln Phe Val Val Arg Asn Gly Lys Arg Leu Pro Ile Gly
 690 695 700
 Gly Gly Thr Glu Ser Leu Gly Ile Trp Asn Lys Thr Glu Pro Gln Trp
 705 710 715 720
 Asn Ala Ala Gly Gly Gly Tyr Thr Glu Val Ser Ser Gly Ser Ser Tyr
 725 730 735
 Ile Gln Ala Val Gly Trp Asp Asp Ser Arg Cys Pro Val Ala Arg Thr
 740 745 750

217770US0PCT.ST25

Leu Leu Thr Tyr Ser Gln Ser Glu Asn Pro Lys Ser Pro His Tyr Ser
755 760 765

Asp Gln Thr Arg Leu Tyr Ala Gly Glu Arg Trp Val Thr Ser Arg Phe
770 775 780

Cys Glu Arg Asp Ile Ala Arg Ser Pro Asp Leu Arg Val Val Arg Val
785 790 795 800

His Glu Arg Arg

<210> 3
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 3

Ser Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly
1 5 10 15

Leu Leu Leu Gly
20

<210> 4
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 4

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro
1 5 10 15

His Ile Val Ala
20

<210> 5
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 5

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro
1 5 10 15

His His Val Ala
20

<210> 6
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide
 <400> 6
 ctstcsgcsg tsatc 15

 <210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 7
 gtggtgsggg atsc 15

 <210> 8
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 8
 csgtsgcstt cgacgg 16

 <210> 9
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 9
 sccsagsags agscc 15

 <210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 10
 atccggtaca cggagtacgg 20

 <210> 11
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 11
 cgttcaccgt cgtggagcc 19

 <210> 12
 <211> 10

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 12
 aattgagctc 10

<210> 13
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 13
 caactgcgcg tagtcc 16

<210> 14
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 14
 catgggttcc aacgcg 16

<210> 15
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 15
 gctgtcaacc gtctgg 16

<210> 16
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 16
 acgcgctgaa cgatcc 16

<210> 17
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 17
 cggacctgga cctacc 16

<210> 18	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic oligonucleotide	
<400> 18	
gtgggtgaac acgatcg	17
<210> 19	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic oligonucleotide	
<400> 19	
gaccttcagc ggcagc	16
<210> 20	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic oligonucleotide	
<400> 20	
caagtgggtgt gcggcg	16
<210> 21	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic oligonucleotide	
<400> 21	
gtcgctgggc atctgg	16
<210> 22	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> synthetic oligonucleotide	
<400> 22	
gctgctgacg tactcc	16
<210> 23	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> synthetic oligonucleotide

<400> 23

gtcaaccgca tgggtcc

16

<210> 24

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 24

atcgcttgga tcgtcg

16

<210> 25

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 25

cgtcagcgcg atcacc

16

<210> 26

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 26

ggtgtacagc agctgc

16

<210> 27

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 27

ctccctcgtc ctgacc

16

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 28

gagttgtgcg cgtagg

16

<210> 29

<211> 16

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 29
 tgacgcttgg ccgtcc 16

<210> 30
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 30
 gactacgcg agttgg 16

<210> 31
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 31
 tacaacgcgt ggatcg 16

<210> 32
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 32
 ggtgatccgg ttctgc 16

<210> 33
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 33
 gggtagtgcg ggttgc 16

<210> 34
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 34
 ctgcatcagc tcagcc 16

<210> 35
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 35
 gtccaccact ggggtgc 16

<210> 36
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 36
 gaagcgggggt aggtgg 16

<210> 37
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 37
 ccggtgctga agaacc 16

<210> 38
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 38
 ctgccgctga aggtcc 16

<210> 39
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 39
 tcgaacggcg tcctcc 16

<210> 40
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic oligonucleotide
 <400> 40
 tggaggacgc cgttcg 16

 <210> 41
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 41
 gcctggatgt agctgg 16

 <210> 42
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 42
 ggacatcgcg cgttcg 16

 <210> 43
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 43
 cgaacgcgcg atgtcc 16

 <210> 44
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 44
 ccgtgaccat gcgtgc 16

 <210> 45
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 45
 gcacgcatgg tcacgg 16

 <210> 46
 <211> 16

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 46
 gaggagacct acctcg 16

<210> 47
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 47
 aggtcccgct acgacg 16

<210> 48
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 48
 gaccatgcgg ttgacg 16

<210> 49
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 49
 cagttccgcc tcgtcg 16

<210> 50
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 50
 caggtggacg ttgtcg 16

<210> 51
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 51
 gtcgctgacg atcacg 16